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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                Database :
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Maximum DB seq length: 2000000000
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                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
%
Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             March 1, 2001, 16:09:29; Search time 299.73 Seconds (without alignments) 23.463 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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342
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sp_phage:*
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sp_rodent:*
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sp_bacteria:*
sp_fungi:*
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sp_unclassified:*
                                        SUMMARIES
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92	92	92.5	93	93.5	94.5	96	100	100	100.5	101.5	103.5	104	113	126.5	127.5	130.5	143.5	342	Score
26.9	26.9	27.0	27.2	27.3	27.6	28.1	29.2	29.2	29.4	29.7	30.3	30.4	33.0	37.0	37.3	38.2	42.0	100.0	Query Match
454	139	838	930	828	420	171	666	523	1556	304	1038	810	2123	666	625	666	593	525	Length
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P91642 drosophila	Q62006 mus musculu	Q9y0c9 dictyosteli	Q9szy9 arabidopsis	Q9vzu6 drosophila	O35861 mus musculu	Q61118 mus musculu	Q9w318 drosophila	Q9ulk4 drosophila	Q9u6al drosophila		O60983 dictyosteli		Q.	Q9spl5 macadamia i	w	Q9sp14 macadamia i	Q9sew4 juglans reg	Q43358 theobroma c	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
86.5	86.5	86.5	87	87	88	88	88	88	88	88	88.5	89	89	89	89	89	. 68	89	90	90.5	91	91	91.5	92	92
25.3	25.3	25.3	25.4	25.4	25.7	25.7	25.7	25.7	25.7	25.7	25.9	26.0	26.0	26.0	26.0	26.0	26.0	26.0	26.3	26.5	26.6	26.6	26.8	26.9	26.9
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Q9w2k6 drosophila		Q9y4jl homo sapien	7		Q23863 dictyosteli	~		വ		081251 zea mays su	Q9w4n4 drosophila	Q9nds4 dictyosteli	_	Q9ntg8 homo sapien	Q9w3al drosophila	Q9kmz5 vibrio chol	087306 borrelia bu	ω	5		9		Q9w4e8 drosophila	O88542 mus musculu	Q9vt57 drosophila

ALIGNMENTS

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RESULT
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ID Q9SPL4
AC Q9SPL4
D7 Q7 Q9SPL4
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Best Local
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01-MAY-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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O9SEW4
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
                                                                                                                                                     EMBL; AF161884; AAD54245.1; HSSP; P02853; 2PHL.
                                                                                                                                                                                                                                             TISSUE=NUT KERNEL;
Marcus J.P., Goulter K.C.,
"A family of antimicrobial
                                                                                                                                                                                                                                                                                                                                                                              Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; Proteace
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMP2
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Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; endicotyledons; core eudicots; Rosidae; eurosids I;

Fagales; Juglandaceae; Juglans.
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VICILIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. SUNLAND: TISSUE-SOMATIC EMBRYO LINE:
Teuber S.S., Jarvis K.C., Peterson W.R., Dandekar A.M., Ansari A.A.;
"Identification and cloning of a cDNA encoding a vicilin-like protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF066055; AAF18269.1; HSSP; P02853; 2PHL.
                                                                                                                                 INTERPRO;
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                                                                                                         PRO; IPR001113; PF00546; Seedst
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                                                                                     Seedstore_7s;
AA; 78243 MW;
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Last sequence update)
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10; Mismatches
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Score
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Q9SPL5;
Q1-MAY-2000
Q1-MAY-2000
Q1-OCT-2000
TISSUE-NUT KERNEL;
Marcus J.P., Goulter K.C., Green J.I
"A family of antimicrobial peptides
globulin protein in Macadamia integr
Plant J. 0:0-0(1999).
EMBL; AF161883; AAD54244.1; -.
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Magnoliophyta; eudicotylec
NCBI_TaxID=60698;
                                                                                                                                                                                 Macadamia integrifolia (Macadamia nut).
Eukaryota; Viridiplantae; Embryophyta; Trav
Magnoliophyta; eudicotyledons; Proteaceae;
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Q1-MAY-2000 (TrEMBLrel. 13,
Q1-CCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                    AMP2
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Eukaryota; Viridiplantae; Embryophyta; Trac
Magnoliophyta; eudicotyledons; Proteaceae;
NCBI_TaxID=60698;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QRQYQQCQGRCQEQQQGQREQQQCQRKC-----WEQYKEQERGEHENYHNHKKN
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) (TrEMBLrel.
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Last annotation updat
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Pred. No. 1.
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des is
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                                                             produced by
                                                                                                                                                                                                        Tracheophyta;
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                                                                                  Manners J
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Best Local :
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                                           Q9ZWI3;
01-MAY-1999
01-MAY-1999
01-OCT-2000
PV100.
Cucurbita maxima (Pumpkin) (Winter squash).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Cucurbitales; Cucurbitaceae; Cucurbita
                                                                                                                                                        2005
                                                                                                                                                                                                                                                   PFAM; PF00072; response_reg; 1.
PFAM; PF0021; guanylate_cyc; 1.
PRINTS; PR00344; BCTRLSENSOR.
PROSITE; PS00387; PPASE; UNKNOWN_1.
SEQUENCE 2123 AA; 243039 MW; 744247140BC342FA CRC64;
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01-MAY-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
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INTERPRO; IPRO01440; -.
INTERPRO; IPRO01596; -.
INTERPRO; IPRO01789; -.
                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAY-1999) to the EMBL; AF153362; AAD50121.1;
                                                                                                                                                                                                                                                                                                                                                                                                 Dictyostelium."
                                                                                                                                                                                                                                                                                                                                                                                                           Soderbom F., Anjard C., Iranfar N., "An adenylyl cyclase that functions
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-AX4
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum (Slime mold) Eukaryota; Dictyosteliida; Dictyostel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9U9S7
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INTERPRO; IPRO01113;
PFAM; PF00546; Seeds
                                                                                                                                                                                                                                                                                                                                                      [NTERPRO;
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nes 20; Conserv
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                                                                                                                                                                        2 QRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGEHENYHNHKKNRSEEEEGQQ
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                                                                                                                                                                                                                                                                                                                                                                P19754; 1AWK.
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                                                     3 (TrEMBLrel. 10, '9 (TrEMBLrel. 10, '0) (TrEMBLrel. 15,
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                                                                                                   PRELIMINARY;
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Last annotation updat
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Pred. No. 0.00
22; Mismatches
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Last annotation update)
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Pred. No. 1.
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Best Local Similarity 37.3
Matches 22; Conservative
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Best Local 9
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O15409;
O15409;
O1-JAN-1998
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060983;
01-AUG-1998
01-AUG-1998
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                     EMBL; AF000580; AAC14390.1; Plasmid. SEQUENCE 1038 AA; 121723
                                                                                                                                                                                                                                                                                                                                                                                              Rieben W.K., Gonzales C., Go
Hughes J.E., Welker D.L.;
Submitted (APR-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Riebben W.K. Jr., Gonzales C.M., Gonzales S.T., Kiyosawa H., Hughes J.E., Welto, D.L.; "Dictyostelium discocideum nuclear plasmid Ddp5 the Ddp1 and Ddp2 plasmid families."; Genetics 148:1117-1125(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamada K., Shimada T., Kondo M., Nishimura M., Hara-Nishimura "Multiple functional proteins are produced by cleaving Asn-Gin of a single precursor by vacuolar processing enzyme.";
J. Biol. Chem. 274.2563-2570(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=44689
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MEDLINE=99107919; PubMed=9891029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-WS2162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98198836; PubMed=9539429;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEQQEQRERREQQEQQEQQE-QQEQQEQQEQQEQQEQQEQQEQQEQREQEEQEEQR 997
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37.3%;
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Pred. No. 0.00
17; Mismatches
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                                                                                                                                                                                                                                                                                                                                     EF24CD47F45BB488 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                          S.T.,
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Best Local S
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Best Local Similarity
                                                                                                                                    Homeobox;
SEQUENCE
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston
Submitted
                                                                                                                                                            Xu C., Kauffmann R.C., Zhang J., Kladny S., Carthew R.W.; "Overlapping activators and repressors delimit transcriptional response to receptor tyrosine kinase signals in the Drosophila Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AF190405; AAF06660.1; -
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MREDLINE=97369492; PubMed=9225980; Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., K Breschel T.S., Stine O.C., Callahan C., Mcinnis M.G., "cDNAs with long CAG trinucleotide repeats from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                   Drosophila virilis (Fruit fly).
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01-NOV-1998
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                                                                                                                                                                                                                                                    NCBI_TaxID=7244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-86 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       151
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 OR
R
                                    QRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQER---GEHENYHNHKKNRSEEEEEGQ
                       QQQQQQQQQQQQQQQQQQQQQQQQQQRRYEQEQEQQRRMEEQQQQLHRQQQHLQQLQQQQ 832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                    DNA-binding; Nuclear protein.
1556 AA; 171029 MW; 6FEACFEA2D73E644 CRC64;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 13, Last annotation update)
TRANSCRIPTION FACTOR PROSPERO.
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                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sutterer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34400 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.7%;
35.0%;
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                                                                    Score 100.5;
Pred. No. 0.00
19; Mismatches
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Last annotation update)
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Pred. No. 0.00054;
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                                                                        18;
                                                                                                                                                                                                                                                                          Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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Addms M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Manaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Dayla A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Berkova D., Botchan M.R., Bouck J., Brokstein P., Botchar A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Chandra I., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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Best Local
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Q9W318;
01-MAY-2000
01-MAY-2000
01-OCT-2000
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Q9U1K4;
Q1-MAY-2000
Q1-MAY-2000
Q1-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=BERKELEY;
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PROSITE; PS00028; ZINC_FINGER_C2H2;
SEQUENCE 523 AA; 54577 MW; 64FB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mech. Dev. 89:1:
EMBL; AJ131022;
HSSP; P08047; 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D-SP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Dro
NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schock F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Neoptera; Endopterygota; Diptera; Brachycera; Musc
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RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Menter C., Melson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Syier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhon M., Zhang G., Zhao Q., Zheng L.,
RA Zheng S.H., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng S.H., Zhong W., Zhan M., Zhang G., Zhao, Zheng L.,
RMBL, Abe003448; Ab46519.1:
DR EMBL, Abe03448; Ab46519.1:
- RMBL, Abe03448; Ab46519.1:
- LEMBL, Abe03448; Ab46519.1:
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Watches 19; Conser
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                                                                                                   EMBL;
                                                                                                                    gene that encodes a nuclear protein comprising and interspersing histidines.";
J. Biol. Chem. 271:25515-25523(1996).
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q61118;
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                                                                                       MGI:108038;
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TE; PS00028; ZINC_FINGER_C2H2;
NCE 666 AA; 67658 MW; 9D4AI
                                                                                                   ol. Chem. 271:25515-2
U46463; AAC52934.1;
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                                                                    C6AA17E6FFB26DE5 CRC64;
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DB 11;
0.0013;
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Q9VZU6; Q24005;
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Q9VZU6; Q24005;
Q1-MAY-2000 (TremBLrel. 13, Last sequence update)
Q1-JUN-2000 (TremBLrel. 14, Last annotation update)
Q1-JUN-2000 (BTB-VII PROTEIN DOMAIN).
 O35861;
O1-JAN-1998 (
O1-JAN-1998 (
O1-OCT-2000 (
 Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muso

Ephydroidea; Drosophilidae; Drosophila.
 SEQUENCE FROM N.A. STRAIN=BERKELEY;
 Adams M.D., Celniker S.E., Holt R.A., E
Amanatides P.G., Scherer S.E., Li P.W.,
 MEDLINE=20196006; PubMed=10731132;
 Genetics 147:1267-1277(1997).
EMBL; U70651; AAC53441.1; -.
HSSP; Q05066; 1HRY.
 misregulation as the cause of
the SRY functional unit.";
 STRAIN=B6JEI-YACH;
MEDLINE=98043417; PubMed=9383069;
 035861
 Adams M.D.,
 SEQUENCE
 Albrecht K.H., Eicher E.M
 SEQUENCE FROM N.A.
 Mammalia; Eutheria;
 Eukaryota; Metazoa;
 Mus musculus
 SEX DETERMINING
 NCBI_TaxID=7227;
 NCBI_TaxID=39442;
 233
 173
 INTERPRO; IPR000910; -.
 "DNA sequence analysis of Sry
 102 QQQ 104
 59
 15
 58
 14
 4 QYQQCQGRCQEQQQGQREQQQC-----QRKCWEQYKEQERGEHENYHNHKKNRSEEEEGQ
 2 QRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKE----QERGEHENYHNHKKNRSEEEEG
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 QQR 60
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 (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.)
 Conservative
 musculus (eastern European
etazoa; Chordata; Craniata;
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 HMG_box;
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 box; 1.
52745 MW;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus
 27.6%;
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 Last sequence update)
Last annotation update)
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 Score
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 alleles (subgenus Mus) implicates C57BL/6J-Y(POS) sex reversal and defines
 PRT;
 4D96FC15559C8212 CRC64;
 Mismatches
 Mismatches
 94.5;
No. 0.
 420
 Evans C.A., Goca
 house mouse).
Vertebrata; Euteleostomi;
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 DB 11;
 18;
 20;
Gocayne J.D.,
.A., Galle R.F.,
 Length
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Search completed: March
Job time: 1575 sec
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Borkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garga N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Munnt S.M., Molson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Munnt S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mang Z.-Y., Wassarman D.A., Keinson J., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Millams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Millams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Rha Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.,
The genome sequence of Drosophila melanogaster.";
RN L Science 287:2185-2195(2000).
 Query Match
Best Local
 Matches
 regulated genes in Drosophila.";
Proc. Natl. Acad. Sci. U.S.A. 91:10717-10721(1994).
EMBL; AE003477; AAF47721.1; -.
 zollman S., Godt D., Prive G.G., Couderc J.L., Laski F.A.; "The BTB domain, found primarily in zinc finger proteins, defines an evolutionarily conserved family that includes several developmentally
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 FLYBASE; F8gn0012049; BtbVII.
 EMBL; U14404; AAA50839.1; -
 MEDLINE-95024186; PubMed-7938017;
 SEQUENCE OF 4-118 FROM N.A.
 NTERPRO;
 Local Similarity hes 17; Conserv
 2 QRQYQQCQGRCQEQQQGQREQQQCQRKCWEQYKEQERGEHENYHNHKKNRSEEEEEGQQ 59
 PF00651;
 IPR000210; -.
 551; BTB; 1.
828 AA; 87135 MW; 19A72E077D570B41 CRC64;
 Conservative
 1,
 27.3%; Score 93.5; DB 5; Length 828; 29.3%; Pred. No. 0.0098;
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